

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)	
)	
Moses CHAO et al.)	Examiner:
)	
Appln. No.: not yet received)	Washington, D.C.
)	
Filed: on even date herewith)	December 19, 2001
)	
For: A TRANSMEMBRANE PROTEIN AS)		Atty. Docket: CHAO=11A
A DOWNSTREAM TARGET OF..)		

PRELIMINARY COMMUNICATION

Honorable Commissioner for Patents
Washington, D.C. 20231

Sir:

The present application as filed includes a paper and computer readable copy of a sequence listing.

I hereby state, in accordance with 37 C.F.R. §1.821(f), that the content of the computer readable copy of the sequence listing is believed to be the same as the paper copy sequence listing which is part of the application as filed.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or

even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

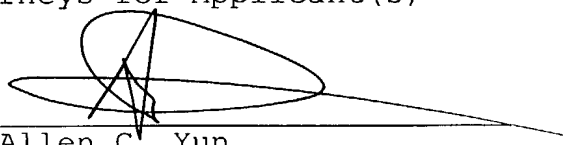
Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above-described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

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By


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